



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cottarel, Guillaume
Damagnez, Veronique
Draetta, Guilo
- (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
Human Pathogens, and Uses Related Thereto
- (iii) NUMBER OF SEQUENCES: 27
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FOLEY, HOAG & ELIOT LLP
 - (B) STREET: One Post Office Square
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02109-2170
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/072,994
 - (B) FILING DATE: 05-MAY-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/463,090
 - (B) FILING DATE: 05-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Vincent, Matthew P.
 - (B) REGISTRATION NUMBER: 36,709
 - (C) REFERENCE/DOCKET NUMBER: MIV-032.02
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-832-1000
 - (B) TELEFAX: 617-832-7000

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1668 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 259..1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGATGATACA AATGTGGAAG ATGCAAATTG TTCTTCCCCT ACTTTGATGA GAAAAAGTGC	60
ATTGAGTAAA ATCATCTTCA AAGGACATTA AACAATAATT CCAAATCACC ATCGCCAACT	120
TTTTCAAATA CAAATGCAAC ATCTGGCTCT CCATTGTCAA ATCTTTCTCG TGCACCATTG	180
AGAAATTTAT CTAATTTTCGT TATTCCTTCG TCAGTTAAAT CAAAACGAA ACAATTTACA	240
AACTCTTTGA CTCGTTCA ATG ACT GAA GTG GTT TCG AAA TCA TCA CAC TCA	291
Met Thr Glu Val Val Ser Lys Ser Ser His Ser	
1 5 10	
TTT TTC AAT AAT TTG CAT CTT GCA ACC TCA ACT GCG TCT TCT TCA GTA	339
Phe Phe Asn Asn Leu His Leu Ala Thr Ser Thr Ala Ser Ser Ser Val	
15 20 25	
TCG AGC ACA ACT CCC AAA ATA GAA TTC AAT TCC ATA GCT GAA AAT GAT	387
Ser Ser Thr Thr Pro Lys Ile Glu Phe Asn Ser Ile Ala Glu Asn Asp	
30 35 40	
GAT ATC CCT ACC AAT TAT GAC TCT GAT GAA GAA TTC GAA GAT GGT GAT	435
Asp Ile Pro Thr Asn Tyr Asp Ser Asp Glu Glu Phe Glu Asp Gly Asp	
45 50 55	
ACG TTT ATA CAA TCC ACC TTG ATT CAC CAG TTC AAC GCA AGT CAA GTA	483
Thr Phe Ile Gln Ser Thr Leu Ile His Gln Phe Asn Ala Ser Gln Val	
60 65 70 75	
ACA ACA ACA ACA ATA ATA ATA ATA CCA ATG ATG GTA ACG ACA ATA ATA	531
Thr Thr Thr Thr Ile Ile Ile Ile Pro Met Met Val Thr Thr Ile Ile	
80 85 90	
TAC CTA CAA AAA TTA GAC GGT TCC ACT CCA TGT ACC AAA CCG ATA AAG	579
Tyr Leu Gln Lys Leu Asp Gly Ser Thr Pro Cys Thr Lys Pro Ile Lys	
95 100 105	
AGA TTG CAT CGT ACC AAC TTC ATG AAG ATA ATT CAT TTT GAA ATT TAC	627
Arg Leu His Arg Thr Asn Phe Met Lys Ile Ile His Phe Glu Ile Tyr	
110 115 120	
AAT ATT GAA TAT TCT CAT CTG GAG AGT GAT TTG TTA CCA CGA ATC GAT	675
Asn Ile Glu Tyr Ser His Leu Glu Ser Asp Leu Leu Pro Arg Ile Asp	
125 130 135	
GCT CAT CAA TTA GCC AGA ATA TTA CGT GGA GAC CAC GAT GAC CAA TTT	723
Ala His Gln Leu Ala Arg Ile Leu Arg Gly Asp His Asp Asp Gln Phe	
140 145 150 155	
GAT GAA TTT ATT ATC ATT GAT TGT CGA TTT GAG TAT GAA TTT AAT GGT	771
Asp Glu Phe Ile Ile Ile Asp Cys Arg Phe Glu Tyr Glu Phe Asn Gly	
160 165 170	

GGC	CAT	ATT	ACT	AGG	GCA	ATC	AAT	ATC	TCC	ACC	CAG	GAA	GCA	CTT	CAA	819
Gly	His	Ile	Thr	Arg	Ala	Ile	Asn	Ile	Ser	Thr	Gln	Glu	Ala	Leu	Gln	
			175					180					185			
GAA	AAG	CTC	TTT	CAA	TAT	CAA	GAA	ACA	GAT	ACC	AAG	GAC	ACT	GAA	AGC	867
Glu	Lys	Leu	Phe	Gln	Tyr	Gln	Glu	Thr	Asp	Thr	Lys	Asp	Thr	Glu	Ser	
		190					195					200				
AAG	AAG	CGA	TTG	ATA	ATT	TTC	CAT	TGT	GAG	TTC	AGT	ATG	TTC	AGA	GGA	915
Lys	Lys	Arg	Leu	Ile	Ile	Phe	His	Cys	Glu	Phe	Ser	Met	Phe	Arg	Gly	
		205				210					215					
CCA	ATG	ATG	GCC	AAA	CAT	TTA	AGA	AAG	TGT	GAT	AGA	ATG	TGC	AAC	TAC	963
Pro	Met	Met	Ala	Lys	His	Leu	Arg	Lys	Cys	Asp	Arg	Met	Cys	Asn	Tyr	
220					225					230					235	
GAC	AAT	TAT	CCT	CTA	TTA	ACA	TAC	CCC	GAT	ATT	GCA	ATT	TTG	GAA	GGA	1011
Asp	Asn	Tyr	Pro	Leu	Leu	Thr	Tyr	Pro	Asp	Ile	Ala	Ile	Leu	Glu	Gly	
			240					245					250			
GGC	TAT	AAG	AAT	TTC	TAT	GAA	AAT	TAC	CCC	CAA	TGG	TGT	GAT	CCT	CAA	1059
Gly	Tyr	Lys	Asn	Phe	Tyr	Glu	Asn	Tyr	Pro	Gln	Trp	Cys	Asp	Pro	Gln	
			255				260						265			
GGA	TAT	GTC	GAG	ATG	AAG	AAT	TTA	CGA	CAC	AAA	AAA	TTA	TGT	GAA	TCC	1107
Gly	Tyr	Val	Glu	Met	Lys	Asn	Leu	Arg	His	Lys	Lys	Leu	Cys	Glu	Ser	
		270					275					280				
AAC	TTG	GAT	AAA	GTT	AGA	AAA	GAT	AAT	AAA	CTA	ACT	AGA	GCA	AAG	TCT	1155
Asn	Leu	Asp	Lys	Val	Arg	Lys	Asp	Asn	Lys	Leu	Thr	Arg	Ala	Lys	Ser	
		285				290					295					
TAT	CAA	TTT	GGT	ATT	CAA	CAC	CGC	CGT	GGT	GGT	TCC	ACT	GGT	GGA	CTT	1203
Tyr	Gln	Phe	Gly	Ile	Gln	His	Arg	Arg	Gly	Gly	Ser	Thr	Gly	Gly	Leu	
300					305				310						315	
TTC	GGC	AAC	TAT	AAT	TAC	AAC	GTT	ATG	AAC	TCA	TCA	GAT	CAA	CAA	TTT	1251
Phe	Gly	Asn	Tyr	Asn	Tyr	Asn	Val	Met	Asn	Ser	Ser	Asp	Gln	Gln	Phe	
				320					325				330			
TGG	AGT	AGC	AGT	ACT	TCC	AAC	ACT	GCT	CAC	CAC	AGA	AGT	AGT	AGC	AGT	1299
Trp	Ser	Ser	Ser	Thr	Ser	Asn	Thr	Ala	His	His	Arg	Ser	Ser	Ser	Ser	
			335					340					345			
AGC	GGG	TTC	ATT	AAT	AAT	ATG	CAT	AGT	GGT	GCT	TCG	TCA	TAT	CAC	CAT	1347
Ser	Gly	Phe	Ile	Asn	Asn	Met	His	Ser	Gly	Ala	Ser	Ser	Tyr	His	His	
		350					355					360				
AGG	TCA	CAA	TCG	TTT	GTA	ACT	ATC	AAT	AAT	GAG	AAA	ATT	ATC	AAG	CGA	1395
Arg	Ser	Gln	Ser	Phe	Val	Thr	Ile	Asn	Asn	Glu	Lys	Ile	Ile	Lys	Arg	
		365				370					375					
CAA	AGA	TCG	ACT	CCC	AAA	GTC	AGC	AAC	TCA	CCA	ACC	AAG	CCA	CCT	CAT	1443
Gln	Arg	Ser	Thr	Pro	Lys	Val	Ser	Asn	Ser	Pro	Thr	Lys	Pro	Pro	His	
380					385					390					395	

CAA CTG TAT CTC CTG ATA AAC CCA TTC CGT TGG CTA ATA TTC ATA GAT	1491
Gln Leu Tyr Leu Leu Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp	
400 405 410	

TAACTCGTGC CAACACTATT TCATCAGACC AAACATTGTT TAGCAATAAG CTGGTATCTT	1551
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CCCCAATGAT ATCTCCACTT GCAGCTAGTT TTGAACAATC GTCGATTGGA ATAAGTTCTT	1611
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CTGAATTATC AGTCAATACT CAAGATTTTC AACCACCGAC TACGTCCTTT AGGAATT	1668
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 208..513

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AACTTGTTTA CTTATTTGTT TATATAATTG ATAGATATCA ATTACTAATT TACCCTTGTT	60
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TTTTACTTCC TACTATTCAA GACTTTATTT CCTCCTGATA ATCATTTTGT TTGATTATCA	120
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TTTTTCGTCAA TTAGTTCTTT TTTTTCATTT GTTTCAGAG TTTAGGAAGA CTACCATTTT	180
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ACAATTTTCA ATTCAAATAT TTTCCCA ATG ACT AAA CCA AGA TTT TTA ACA	231
Met Thr Lys Pro Arg Phe Leu Thr	
1 5	

AGA TAT AGA AAG AGC AAA AGT GTT GGA ATT TCA GAT ATG ATC CAT TAC	279
Arg Tyr Arg Lys Ser Lys Ser Val Gly Ile Ser Asp Met Ile His Tyr	
10 15 20	

AGT CCC AGA TAC AGT GAT GAT TCA TAC GAG TAT AGA CAT GTG ATG TTA	327
Ser Pro Arg Tyr Ser Asp Asp Ser Tyr Glu Tyr Arg His Val Met Leu	
25 30 35 40	

CCC AAG AAT ATG TTG AAA GCA ATT CCT CAC GAT TAC TTT AAT CAA GAA	375
Pro Lys Asn Met Leu Lys Ala Ile Pro His Asp Tyr Phe Asn Gln Glu	
45 50 55	

ACA GGT ACT TTG AGG ATA TTG ACA GAA GAA GAA TGG AGA GGG TTA GGA	423
Thr Gly Thr Leu Arg Ile Leu Thr Glu Glu Glu Trp Arg Gly Leu Gly	
60 65 70	

ATC ACA CAA TCT TTG GGT TGG GCC CAT TAC GAA ACT CAT GCT CCA GAG	471
Ile Thr Gln Ser Leu Gly Trp Ala His Tyr Glu Thr His Ala Pro Glu	
75 80 85	
CCT CAT ATA TTA TTA TTC AAG AGA CCC TTA AAT CCC GGG CAA	513
Pro His Ile Leu Leu Phe Lys Arg Pro Leu Asn Pro Gly Gln	
90 95 100	
TAAAAAGATT AACTATATTT GAATACTATA GAATCGGAAT CGGTTTTAAA GTTAACACTG	573
GAATTAAAAC ATAAAAAGGA AAGAAATAGC CCATTGGTCA CAGTAATCTG TTTCCAACAA	633
CCCCCCTCCT CAGAAATAGG ATAGAAATGA ATTAACGATG AATTTGTATA CACTATTTAT	693
AAGCCAATCT CATTGATTGC ATTTCTTATT TGTATATTAT TAAATACGTA TATCGCGAGA	753
AACTGTATAA ATACTCTTGG TACCTCGCAT GTT	786

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1002 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 43..993

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAGAACACAC ACATCCCAAG CCAAGACCAA CACTTATTGC AA ATG GTA GAG TTA	54
Met Val Glu Leu	
1	
TCT GAT TAT CAA CGT CAA GAA AAA GTC GGA GAA GGT ACT TAT GGG GTT	102
Ser Asp Tyr Gln Arg Gln Glu Lys Val Gly Glu Gly Thr Tyr Gly Val	
5 10 15 20	
GTT TAT AAA GCA TTA GAT ACC AAG CAC AAT AAT AGA GTT GTT GCA TTA	150
Val Tyr Lys Ala Leu Asp Thr Lys His Asn Asn Arg Val Val Ala Leu	
25 30 35	
AAG AAA ATT CGA TTA GAA TCA GAA GAT GAA GGT GTA CCT AGT ACC GCC	198
Lys Lys Ile Arg Leu Glu Ser Glu Asp Glu Gly Val Pro Ser Thr Ala	
40 45 50	
ATT AGA GAA ATC TCG TTA TTA AAA GAA ATG AAA GAT GAT AAT ATC GTT	246
Ile Arg Glu Ile Ser Leu Leu Lys Glu Met Lys Asp Asp Asn Ile Val	
55 60 65	

CGA	TTA	TAT	GAT	ATT	ATT	CAT	TCA	GAT	TCT	CAT	AAA	TTA	TAT	TTA	GTA	294
Arg	Leu	Tyr	Asp	Ile	Ile	His	Ser	Asp	Ser	His	Lys	Leu	Tyr	Leu	Val	
	70					75					80					
TTT	GAA	TTT	TTG	GAT	TTA	GAT	TTA	AAG	AAA	TAT	ATG	GAA	AGT	ATT	CCT	342
Phe	Glu	Phe	Leu	Asp	Leu	Asp	Leu	Lys	Lys	Tyr	Met	Glu	Ser	Ile	Pro	
85					90					95					100	
CAA	GGA	GTT	GGA	CTA	GGG	GCT	AAT	ATG	ATA	AAA	AGA	TTT	ATG	AAT	CAA	390
Gln	Gly	Val	Gly	Leu	Gly	Ala	Asn	Met	Ile	Lys	Arg	Phe	Met	Asn	Gln	
				105					110					115		
TTA	ATT	CGA	GGT	ATT	AAA	CAT	TGT	CAT	TCT	CAT	CGA	GTT	TTA	CAT	CGT	438
Leu	Ile	Arg	Gly	Ile	Lys	His	Cys	His	Ser	His	Arg	Val	Leu	His	Arg	
			120					125					130			
GAT	TTA	AAA	CCA	CAA	AAT	TTA	TTG	ATT	GAT	AAA	GAA	GGG	AAT	TTA	AAA	486
Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asp	Lys	Glu	Gly	Asn	Leu	Lys	
		135					140					145				
TTA	GCA	GAT	TTT	GGA	TTA	GCT	CGA	GCA	TTT	GGA	GTT	CCA	TTA	AGA	GCA	534
Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	Pro	Leu	Arg	Ala	
	150					155					160					
TAT	ACT	CAT	GAA	GTT	GTC	ACT	TTA	TGG	TAT	CGA	GCT	CCC	GAA	ATC	TTG	582
Tyr	Thr	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	
165					170					175					180	
TTA	GGA	GGG	AAA	CAA	TAT	TCC	ACT	GGG	GTA	GAT	ATG	TGG	TCT	GTT	GGA	630
Leu	Gly	Gly	Lys	Gln	Tyr	Ser	Thr	Gly	Val	Asp	Met	Trp	Ser	Val	Gly	
			185					190						195		
TGT	ATA	TTT	GCT	GAA	ATG	TGT	AAT	AGG	AAA	CCA	TTA	TTT	CCT	GGT	GAT	678
Cys	Ile	Phe	Ala	Glu	Met	Cys	Asn	Arg	Lys	Pro	Leu	Phe	Pro	Gly	Asp	
			200					205					210			
TCA	GAA	ATT	GAT	GAA	ATT	TTC	CGA	ATT	TTC	CGA	ATT	TTA	GGA	ACA	CCT	726
Ser	Glu	Ile	Asp	Glu	Ile	Phe	Arg	Ile	Phe	Arg	Ile	Leu	Gly	Thr	Pro	
		215					220					225				
AAT	GAA	GAA	ATT	TGG	CCT	GAT	GTT	AAT	TAT	TTA	CCA	GAT	TTT	AAA	TCA	774
Asn	Glu	Glu	Ile	Trp	Pro	Asp	Val	Asn	Tyr	Leu	Pro	Asp	Phe	Lys	Ser	
	230					235					240					
AGT	TTC	CCT	CAA	TGG	AAA	AAG	AAA	CCT	TTG	AGT	GAA	GCA	GTT	CCA	AGT	822
Ser	Phe	Pro	Gln	Trp	Lys	Lys	Lys	Pro	Leu	Ser	Glu	Ala	Val	Pro	Ser	
245					250					255					260	
TTG	GAT	GCT	AAT	GGA	ATT	GAT	CTT	TTG	GAT	CAA	ATG	TTG	GTG	TAT	GAT	870
Leu	Asp	Ala	Asn	Gly	Ile	Asp	Leu	Leu	Asp	Gln	Met	Leu	Val	Tyr	Asp	
				265					270					275		
CCA	AGT	AGA	AGA	ATA	AGT	GCT	AAA	CGA	GCT	TTA	ATT	CAT	CCT	TAT	TTT	918
Pro	Ser	Arg	Arg	Ile	Ser	Ala	Lys	Arg	Ala	Leu	Ile	His	Pro	Tyr	Phe	
			280					285					290			

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1752 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 184..1659
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GCTATTCCCC CCTTTTCCTT TTTTTTATAG AGAAACTTAT TCCAATTACT CATCGAACAA															60	
GATCTTACTA GACTTGTAGA CTCACGACAC GATAAATTTT AATTCATTAA TCAACCAACG															120	
AACCAGCCAA ACCAAAATTA ATTCACATTT ATACTCACTG TTTGTCATTT TCATCTCATA															180	
GTA	ATG	CCA	CAA	GTC	ACT	AAA	ACT	AAT	AAT	GAA	AAT	GAG	TTT	AGA	CTT	228
Met	Pro	Gln	Val	Thr	Lys	Thr	Asn	Asn	Glu	Asn	Glu	Phe	Arg	Leu		
1				5					10					15		
ACT AGA TCA AAA GTA CAG CAT CAA GAG TCG ATA AGT ACC ATC AAA AAT															276	
Thr	Arg	Ser	Lys	Val	Gln	His	Gln	Glu	Ser	Ile	Ser	Thr	Ile	Lys	Asn	
				20				25						30		
ACG ACC ATA TCC AAT TCT CAG CAT AAA CAA CAA ACA CAA CAA CAA ATT															324	
Thr	Thr	Ile	Ser	Asn	Ser	Gln	His	Lys	Gln	Gln	Thr	Gln	Gln	Gln	Ile	
			35					40					45			
TCA TCA CCA CCT CAA GTC TCT GTA ACA TCA TCT GAA GGA GTT TCA CAT															372	
Ser	Ser	Pro	Pro	Gln	Val	Ser	Val	Thr	Ser	Ser	Glu	Gly	Val	Ser	His	
		50					55					60				
GTC AAT ACA CGT CAA TAT TTG GGT GAT GTT TCA AAT CAA TAC ATA ACA															420	
Val	Asn	Thr	Arg	Gln	Tyr	Leu	Gly	Asp	Val	Ser	Asn	Gln	Tyr	Ile	Thr	
	65					70					75					
AAT GCT AAA CCA ACA AAT AAA AGA AAA CCA TTG GGT GGA GAC AAT GCC															468	
Asn	Ala	Lys	Pro	Thr	Asn	Lys	Arg	Lys	Pro	Leu	Gly	Gly	Asp	Asn	Ala	
80					85					90					95	

CCT	CTA	CAA	AAA	CAA	CAG	CAT	AGA	CCA	TCT	AGA	CCA	ATA	CCC	ATT	GCC	516
Pro	Leu	Gln	Lys	Gln	Gln	His	Arg	Pro	Ser	Arg	Pro	Ile	Pro	Ile	Ala	
				100					105					110		
AGT	GAT	AAC	AAC	AAT	AAT	GGT	AGT	ACC	AGT	AGC	AGT	AGC	AAC	AGT	AGC	564
Ser	Asp	Asn	Asn	Asn	Asn	Gly	Ser	Thr	Ser	Ser	Ser	Ser	Asn	Ser	Ser	
			115					120					125			
AAC	AAC	AAT	AAC	AAC	GAC	GCA	AAT	AGA	CTA	GCA	TCT	TTG	GCA	GTT	CCA	612
Asn	Asn	Asn	Asn	Asn	Asp	Ala	Asn	Arg	Leu	Ala	Ser	Leu	Ala	Val	Pro	
			130					135				140				
TCT	CGA	TTA	CCC	CAA	AAA	CGA	CAA	GCT	ACT	GAA	TCG	TCG	ACA	AAT	TTA	660
Ser	Arg	Leu	Pro	Gln	Lys	Arg	Gln	Ala	Thr	Glu	Ser	Ser	Thr	Asn	Leu	
	145					150					155					
GTA	GAG	AAA	TTA	AGA	GTA	CCA	CAA	CCA	GAA	GTA	GGG	GAA	AGA	AGT	CAG	708
Val	Glu	Lys	Leu	Arg	Val	Pro	Gln	Pro	Glu	Val	Gly	Glu	Arg	Ser	Gln	
160					165					170					175	
TCA	TAC	CAT	AAG	AAA	TCA	CGT	TTA	ATT	GAT	TAT	GAA	TGG	CAG	GAT	TTG	756
Ser	Tyr	His	Lys	Lys	Ser	Arg	Leu	Ile	Asp	Tyr	Glu	Trp	Gln	Asp	Leu	
				180					185					190		
GAT	GAA	GAA	GAT	AAT	GAC	GAC	CAA	TTA	ATG	GTT	AGT	GAA	TAT	GTT	AAC	804
Asp	Glu	Glu	Asp	Asn	Asp	Asp	Gln	Leu	Met	Val	Ser	Glu	Tyr	Val	Asn	
			195					200					205			
GAA	ATA	TTT	TCG	TAC	TAT	TAC	GAA	TTA	GAA	ACA	CGA	ATG	TTA	CCT	GAT	852
Glu	Ile	Phe	Ser	Tyr	Tyr	Tyr	Glu	Leu	Glu	Thr	Arg	Met	Leu	Pro	Asp	
		210					215					220				
CCG	CAA	TAT	CTT	TTC	AAA	CAA	ACA	TTG	TTA	AAA	CCA	AGA	ATG	AGA	TCG	900
Pro	Gln	Tyr	Leu	Phe	Lys	Gln	Thr	Leu	Leu	Lys	Pro	Arg	Met	Arg	Ser	
	225					230					235					
ATA	TTG	GTT	GAT	TGG	CTT	GTT	GAA	ATG	CAT	TTA	AAA	TTC	AAG	TTA	TTA	948
Ile	Leu	Val	Asp	Trp	Leu	Val	Glu	Met	His	Leu	Lys	Phe	Lys	Leu	Leu	
240					245					250					255	
CCT	GAA	TCA	CTT	TTT	TTG	GCA	GTC	AAT	GTA	ATG	GAT	AGA	TTC	ATG	TCT	996
Pro	Glu	Ser	Leu	Phe	Leu	Ala	Val	Asn	Val	Met	Asp	Arg	Phe	Met	Ser	
				260					265					270		
GTT	GAA	GTG	GTT	CAA	ATA	GAT	AAA	TTA	CAA	TTA	TTG	GCT	ACA	GCA	GCT	1044
Val	Glu	Val	Val	Gln	Ile	Asp	Lys	Leu	Gln	Leu	Leu	Ala	Thr	Ala	Ala	
			275					280					285			
TTA	TTT	ACT	GCT	GCC	AAA	AAT	GAA	GAA	GTA	TTT	TCT	CCC	CTG	GTT	AAA	1092
Leu	Phe	Thr	Ala	Ala	Lys	Asn	Glu	Glu	Val	Phe	Ser	Pro	Leu	Val	Lys	
		290					295					300				
AAT	TAT	GCA	TAT	TTC	ACT	GAT	GGT	TCA	TAT	ACT	CCA	GAA	GAA	GTG	GTA	1140
Asn	Tyr	Ala	Tyr	Phe	Thr	Asp	Gly	Ser	Tyr	Thr	Pro	Glu	Glu	Val	Val	
	305					310					315					

CAA GCA GAA AAA TAC ATG CTT ACC ATT CTT AAC TTT GAT TTG AAT TAC Gln Ala Glu Lys Tyr Met Leu Thr Ile Leu Asn Phe Asp Leu Asn Tyr 320 325 330 335	1188
CCC AAT CCA ATG AAT TTC TTG AGA AGA ATT TCT AAA GCT GAT GAT TAT Pro Asn Pro Met Asn Phe Leu Arg Arg Ile Ser Lys Ala Asp Asp Tyr 340 345 350	1236
GAT GTC CAA TCA AGA ACG CTA GGA AAA TAT CTT TTG GAA ATC ACT ATA Asp Val Gln Ser Arg Thr Leu Gly Lys Tyr Leu Leu Glu Ile Thr Ile 355 360 365	1284
GTT GAT TAC AAA TTT ATT GGT ATG AGA CCA TCT TTA TGT TGT GCC CTG Val Asp Tyr Lys Phe Ile Gly Met Arg Pro Ser Leu Cys Cys Ala Leu 370 375 380	1332
GCC ATG TAT TTA GCA AGA CTA ATA TTG GGC AAA TTG CCA GTT TGG AAT Ala Met Tyr Leu Ala Arg Leu Ile Leu Gly Lys Leu Pro Val Trp Asn 385 390 395	1380
GGG AAT TTG ATT CAT TAT AGT GGA GGT TAT AGA ATC AGT GAT ATG AGA Gly Asn Leu Ile His Tyr Ser Gly Gly Tyr Arg Ile Ser Asp Met Arg 400 405 410 415	1428
GAA TGT ATC GAA TTA ATG TTT CAA TAT CTT ATT GCT CCT ATA GAA CAT Glu Cys Ile Glu Leu Met Phe Gln Tyr Leu Ile Ala Pro Ile Glu His 420 425 430	1476
GAT GAA TTT TTC AAA AAA TAT GCC ATG AGA AAA TTT ATG AGA GCA AGT Asp Glu Phe Phe Lys Lys Tyr Ala Met Arg Lys Phe Met Arg Ala Ser 435 440 445	1524
ACT CTT TGT CGA AAT TGG GCT AAA AAA TTC CAA GCA TCA GGA AGA GAT Thr Leu Cys Arg Asn Trp Ala Lys Lys Phe Gln Ala Ser Gly Arg Asp 450 455 460	1572
TTG TTT GAT GAA CGA TTA TCG ACC CAT AGG CTA ACA TTA GAA GAT GAT Leu Phe Asp Glu Arg Leu Ser Thr His Arg Leu Thr Leu Glu Asp Asp 465 470 475	1620
GAC GAA GAA GAA GAA ATA GTG GTA GCA GAA GCA GAA GAG TAAAGTTTGTG Asp Glu Glu Glu Glu Ile Val Val Ala Glu Ala Glu Glu 480 485 490	1669
AGGACTATTG GATCTAGGTT CTTATCTTTA CAATGCATAA ATGAGGAAAT GAAAGAAGAT	1729
GAACATGAGT TATGTGCATT ACC	1752

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1070 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..1058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATCAAATCCA TCAGAGAACC ACATCAATC	ATG TCT ACT GCA GCA GTT GCA ACG	53
	Met Ser Thr Ala Ala Val Ala Thr	
	1 5	
AAA CCA TCT GTC ACT TCA AAA CCA GCA ACT AAA CAA GTT CTG AAT TAC	101	
Lys Pro Ser Val Thr Ser Lys Pro Ala Thr Lys Gln Val Leu Asn Tyr		
10 15 20		
ACC AAA GAA AAA AAA GTA GGG GAA GGT ACA TAT GCT GTT GTG TAC TTG	149	
Thr Lys Glu Lys Lys Val Gly Glu Gly Thr Tyr Ala Val Val Tyr Leu		
25 30 35 40		
GGT AAA CAA ATC TCC ACC AAA CGT CAA ATT GCC ATC AAA GAA ATC AAA	197	
Gly Lys Gln Ile Ser Thr Lys Arg Gln Ile Ala Ile Lys Glu Ile Lys		
45 50 55		
ACA GGA TTA TTC AAA GAT GGG TTG GAT ATG TCA GCA TTG AGA GAA GTG	245	
Thr Gly Leu Phe Lys Asp Gly Leu Asp Met Ser Ala Leu Arg Glu Val		
60 65 70		
AAA TAT TTG CAA GAA TTG AAA CAT CCC AAT GTT ATT GAA CTA GTA GAT	293	
Lys Tyr Leu Gln Glu Leu Lys His Pro Asn Val Ile Glu Leu Val Asp		
75 80 85		
GTA TTT TCA GCA ACA AAT AAT TTA AAT TTG GTA TTA GAA TTT CTA CCT	341	
Val Phe Ser Ala Thr Asn Asn Leu Asn Leu Val Leu Glu Phe Leu Pro		
90 95 100		
TGC GAT TTG GAA GTG TTG ATC AAA GAT AAA TCG ATT GTT TTC AAA TCA	389	
Cys Asp Leu Glu Val Leu Ile Lys Asp Lys Ser Ile Val Phe Lys Ser		
105 110 115 120		
GCA GAT ATC AAA TCA TGG CTT TTA ATG ACA TTA CGT GGG ATA CAT CAT	437	
Ala Asp Ile Lys Ser Trp Leu Leu Met Thr Leu Arg Gly Ile His His		
125 130 135		
TGT CAT CGG AAT TTT ATT TTA CAT CGT GAT TTG AAA CCA AAT AAT TTA	485	
Cys His Arg Asn Phe Ile Leu His Arg Asp Leu Lys Pro Asn Asn Leu		
140 145 150		
TTA TTG GCA CCG GAT GGA CAA TTG AAA ATA GCG GAT TTT GGT CTT GCA	533	
Leu Leu Ala Pro Asp Gly Gln Leu Lys Ile Ala Asp Phe Gly Leu Ala		
155 160 165		
CGA GCT TTG GTA AAT CCT AAT GAA GAT TTA TCA TCT AAT GTT GTC ACT	581	
Arg Ala Leu Val Asn Pro Asn Glu Asp Leu Ser Ser Asn Val Val Thr		
170 175 180		

AGA TGG TAT AGA GCC CCT GAA TTA TTA TTT GGT GCT CGA CAT TAC ACT	629
Arg Trp Tyr Arg Ala Pro Glu Leu Leu Phe Gly Ala Arg His Tyr Thr	
185 190 195 200	
GGA GCA GTT GAT ATC TGG TCA ATA GGT ATA ATA TTT GCT GAA TTA ATG	677
Gly Ala Val Asp Ile Trp Ser Ile Gly Ile Ile Phe Ala Glu Leu Met	
205 210 215	
CTT CGA ATA CCT TAT TTG CCA GGT AAA GAT GAC GTT GAT CAA TTA GAT	725
Leu Arg Ile Pro Tyr Leu Pro Gly Lys Asp Asp Val Asp Gln Leu Asp	
220 225 230	
GTT ACA TTT AGA GCT TAT GGG ACA CCA ACA GAG CAA ATA TGG CCA AAT	773
Val Thr Phe Arg Ala Tyr Gly Thr Pro Thr Glu Gln Ile Trp Pro Asn	
235 240 245	
GTT TCC AGT TTG CCA ATG TAT AAT GCA CTT CAT GTG TAT CCA CCT CCT	821
Val Ser Ser Leu Pro Met Tyr Asn Ala Leu His Val Tyr Pro Pro Pro	
250 255 260	
TCA AGA CAA GAA TTA CGT AAT AGA TTT AGT GCT GCT ACG GAA AAA GCC	869
Ser Arg Gln Glu Leu Arg Asn Arg Phe Ser Ala Ala Thr Glu Lys Ala	
265 270 275 280	
CTT GAT TTG TTG ATA TCG ATG ACC CAA TTG GAT CCA AGT AGA AGA TGT	917
Leu Asp Leu Leu Ile Ser Met Thr Gln Leu Asp Pro Ser Arg Arg Cys	
285 290 295	
GAT TCT ACA CTA GCA TTA TTA CAC GAT TAT TTT ACT GAA TCG CCT CGT	965
Asp Ser Thr Leu Ala Leu Leu His Asp Tyr Phe Thr Glu Ser Pro Arg	
300 305 310	
CCT ACT GAC CCG AAA AAG TTG CCT AAA AAG TCT TCT CCA GAA AAG AGA	1013
Pro Thr Asp Pro Lys Lys Leu Pro Lys Lys Ser Ser Pro Glu Lys Arg	
315 320 325	
GAA AAT GAA GAT GAA CAG AAT AAT GGC TCT AAA AGA AGG CAT GTT	1058
Glu Asn Glu Asp Glu Gln Asn Asn Gly Ser Lys Arg Arg His Val	
330 335 340	
TAGGTTTCTA TA	1070

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGT	TCA	GCT	ATT	GAT	ACG	AAA	AGT	TCA	GTC	TCA	GCG	ATG	GAG	CAC	AAG	48
Cys	Ser	Ala	Ile	Asp	Thr	Lys	Ser	Ser	Val	Ser	Ala	Met	Glu	His	Lys	
1				5					10					15		
ATT	GCT	ATA	AAG	AAA	GTA	ACA	AAG	ATT	TTC	AAC	AAA	GAC	ATC	CTT	CTA	96
Ile	Ala	Ile	Lys	Lys	Val	Thr	Lys	Ile	Phe	Asn	Lys	Asp	Ile	Leu	Leu	
			20					25					30			
ATC	AGG	GCA	ATA	CGA	GAG	CTT	AAG	TTC	ATG	ATG	TTT	TTC	AGA	GGC	CAC	144
Ile	Arg	Ala	Ile	Arg	Glu	Leu	Lys	Phe	Met	Met	Phe	Phe	Arg	Gly	His	
		35					40					45				
AAG	AAT	ATT	GCA	ACT	TTG	CTT	GAC	TTA	GAT	GTT	GTA	TAT	GTG	AAG	CCT	192
Lys	Asn	Ile	Ala	Thr	Leu	Leu	Asp	Leu	Asp	Val	Val	Tyr	Val	Lys	Pro	
	50					55					60					
TAT	GAA	GGC	TTG	TAT	TGT	TTT	CAA	GAG	CTA	GCC	GAT	TTA	GAT	TTA	GCT	240
Tyr	Glu	Gly	Leu	Tyr	Cys	Phe	Gln	Glu	Leu	Ala	Asp	Leu	Asp	Leu	Ala	
65					70				75						80	
CGT	GTT	TTG	TAC	TCA	AAC	GTC	CAA	TTT	TCA	GAA	TTT	CAC	ATT	CAA	AGC	288
Arg	Val	Leu	Tyr	Ser	Asn	Val	Gln	Phe	Ser	Glu	Phe	His	Ile	Gln	Ser	
				85					90					95		
TTT	ATG	TAC	CAA	ATT	CTT	TGC	GGA	CTC	AAG	TAC	ATC	CAT	TCT	GCT	GAT	336
Phe	Met	Tyr	Gln	Ile	Leu	Cys	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asp	
			100					105					110			
GTA	ATA	CAT	CGG	GAC	CTA	AAG	CCA	GGA	AAC	ATA	TTG	GTC	ACC	ACT	CAA	384
Val	Ile	His	Arg	Asp	Leu	Lys	Pro	Gly	Asn	Ile	Leu	Val	Thr	Thr	Gln	
		115					120					125				
GGG	ACT	TTA	AAA	ATA	TGT	GAT	TTC	GGC	TTA	GCA	CGA	GGA	ATA	AAT	CCT	432
Gly	Thr	Leu	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Gly	Ile	Asn	Pro	
	130					135					140					
GTA	TAT	TTC	AGA	AAC	CGC	TCA	GCT	GTC	ATC	ACA	AAC	TAC	GTA	GCA		477
Val	Tyr	Phe	Arg	Asn	Arg	Ser	Ala	Val	Ile	Thr	Asn	Tyr	Val	Ala		
145					150				155							

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Thr	Glu	Val	Val	Ser	Lys	Ser	Ser	His	Ser	Phe	Phe	Asn	Asn	Leu
1				5					10					15	

His	Leu	Ala	Thr	Ser	Thr	Ala	Ser	Ser	Ser	Val	Ser	Ser	Thr	Thr	Pro
			20					25					30		
Lys	Ile	Glu	Phe	Asn	Ser	Ile	Ala	Glu	Asn	Asp	Asp	Ile	Pro	Thr	Asn
		35					40					45			
Tyr	Asp	Ser	Asp	Glu	Glu	Phe	Glu	Asp	Gly	Asp	Thr	Phe	Ile	Gln	Ser
	50					55					60				
Thr	Leu	Ile	His	Gln	Phe	Asn	Ala	Ser	Gln	Val	Thr	Thr	Thr	Thr	Ile
65					70					75					80
Ile	Ile	Ile	Pro	Met	Met	Val	Thr	Thr	Ile	Ile	Tyr	Leu	Gln	Lys	Leu
				85					90					95	
Asp	Gly	Ser	Thr	Pro	Cys	Thr	Lys	Pro	Ile	Lys	Arg	Leu	His	Arg	Thr
			100					105					110		
Asn	Phe	Met	Lys	Ile	Ile	His	Phe	Glu	Ile	Tyr	Asn	Ile	Glu	Tyr	Ser
		115					120					125			
His	Leu	Glu	Ser	Asp	Leu	Leu	Pro	Arg	Ile	Asp	Ala	His	Gln	Leu	Ala
		130				135					140				
Arg	Ile	Leu	Arg	Gly	Asp	His	Asp	Asp	Gln	Phe	Asp	Glu	Phe	Ile	Ile
145					150					155					160
Ile	Asp	Cys	Arg	Phe	Glu	Tyr	Glu	Phe	Asn	Gly	Gly	His	Ile	Thr	Arg
				165					170					175	
Ala	Ile	Asn	Ile	Ser	Thr	Gln	Glu	Ala	Leu	Gln	Glu	Lys	Leu	Phe	Gln
			180					185					190		
Tyr	Gln	Glu	Thr	Asp	Thr	Lys	Asp	Thr	Glu	Ser	Lys	Lys	Arg	Leu	Ile
		195					200					205			
Ile	Phe	His	Cys	Glu	Phe	Ser	Met	Phe	Arg	Gly	Pro	Met	Met	Ala	Lys
	210					215					220				
His	Leu	Arg	Lys	Cys	Asp	Arg	Met	Cys	Asn	Tyr	Asp	Asn	Tyr	Pro	Leu
225					230					235					240
Leu	Thr	Tyr	Pro	Asp	Ile	Ala	Ile	Leu	Glu	Gly	Gly	Tyr	Lys	Asn	Phe
				245					250					255	
Tyr	Glu	Asn	Tyr	Pro	Gln	Trp	Cys	Asp	Pro	Gln	Gly	Tyr	Val	Glu	Met
			260					265					270		
Lys	Asn	Leu	Arg	His	Lys	Lys	Leu	Cys	Glu	Ser	Asn	Leu	Asp	Lys	Val
		275					280					285			
Arg	Lys	Asp	Asn	Lys	Leu	Thr	Arg	Ala	Lys	Ser	Tyr	Gln	Phe	Gly	Ile
	290					295					300				
Gln	His	Arg	Arg	Gly	Gly	Ser	Thr	Gly	Gly	Leu	Phe	Gly	Asn	Tyr	Asn
305					310					315					320

Tyr Asn Val Met Asn Ser Ser Asp Gln Gln Phe Trp Ser Ser Ser Thr
 325 330 335
 Ser Asn Thr Ala His His Arg Ser Ser Ser Ser Gly Phe Ile Asn
 340 345 350
 Asn Met His Ser Gly Ala Ser Ser Tyr His His Arg Ser Gln Ser Phe
 355 360 365
 Val Thr Ile Asn Asn Glu Lys Ile Ile Lys Arg Gln Arg Ser Thr Pro
 370 375 380
 Lys Val Ser Asn Ser Pro Thr Lys Pro Pro His Gln Leu Tyr Leu Leu
 385 390 395 400
 Ile Asn Pro Phe Arg Trp Leu Ile Phe Ile Asp
 405 410

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Thr Lys Pro Arg Phe Leu Thr Arg Tyr Arg Lys Ser Lys Ser Val
 1 5 10 15
 Gly Ile Ser Asp Met Ile His Tyr Ser Pro Arg Tyr Ser Asp Asp Ser
 20 25 30
 Tyr Glu Tyr Arg His Val Met Leu Pro Lys Asn Met Leu Lys Ala Ile
 35 40 45
 Pro His Asp Tyr Phe Asn Gln Glu Thr Gly Thr Leu Arg Ile Leu Thr
 50 55 60
 Glu Glu Glu Trp Arg Gly Leu Gly Ile Thr Gln Ser Leu Gly Trp Ala
 65 70 75 80
 His Tyr Glu Thr His Ala Pro Glu Pro His Ile Leu Leu Phe Lys Arg
 85 90 95
 Pro Leu Asn Pro Gly Gln
 100

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Val	Glu	Leu	Ser	Asp	Tyr	Gln	Arg	Gln	Glu	Lys	Val	Gly	Glu	Gly	1	5	10	15
Thr	Tyr	Gly	Val	Val	Tyr	Lys	Ala	Leu	Asp	Thr	Lys	His	Asn	Asn	Arg	20	25	30	
Val	Val	Ala	Leu	Lys	Lys	Ile	Arg	Leu	Glu	Ser	Glu	Asp	Glu	Gly	Val	35	40	45	
Pro	Ser	Thr	Ala	Ile	Arg	Glu	Ile	Ser	Leu	Leu	Lys	Glu	Met	Lys	Asp	50	55	60	
Asp	Asn	Ile	Val	Arg	Leu	Tyr	Asp	Ile	Ile	His	Ser	Asp	Ser	His	Lys	65	70	75	80
Leu	Tyr	Leu	Val	Phe	Glu	Phe	Leu	Asp	Leu	Asp	Leu	Lys	Lys	Tyr	Met	85	90	95	
Glu	Ser	Ile	Pro	Gln	Gly	Val	Gly	Leu	Gly	Ala	Asn	Met	Ile	Lys	Arg	100	105	110	
Phe	Met	Asn	Gln	Leu	Ile	Arg	Gly	Ile	Lys	His	Cys	His	Ser	His	Arg	115	120	125	
Val	Leu	His	Arg	Asp	Leu	Lys	Pro	Gln	Asn	Leu	Leu	Ile	Asp	Lys	Glu	130	135	140	
Gly	Asn	Leu	Lys	Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Phe	Gly	Val	145	150	155	160
Pro	Leu	Arg	Ala	Tyr	Thr	His	Glu	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	165	170	175	
Pro	Glu	Ile	Leu	Leu	Gly	Gly	Lys	Gln	Tyr	Ser	Thr	Gly	Val	Asp	Met	180	185	190	
Trp	Ser	Val	Gly	Cys	Ile	Phe	Ala	Glu	Met	Cys	Asn	Arg	Lys	Pro	Leu	195	200	205	
Phe	Pro	Gly	Asp	Ser	Glu	Ile	Asp	Glu	Ile	Phe	Arg	Ile	Phe	Arg	Ile	210	215	220	
Leu	Gly	Thr	Pro	Asn	Glu	Glu	Ile	Trp	Pro	Asp	Val	Asn	Tyr	Leu	Pro	225	230	235	240
Asp	Phe	Lys	Ser	Ser	Phe	Pro	Gln	Trp	Lys	Lys	Lys	Pro	Leu	Ser	Glu	245	250	255	
Ala	Val	Pro	Ser	Leu	Asp	Ala	Asn	Gly	Ile	Asp	Leu	Leu	Asp	Gln	Met	260	265	270	
Leu	Val	Tyr	Asp	Pro	Ser	Arg	Arg	Ile	Ser	Ala	Lys	Arg	Ala	Leu	Ile	275	280	285	

His Pro Tyr Phe Asn Asp Asn Asp Asp Arg Asp His Asn Asn Tyr Asn
290 295 300

Glu Asp Asn Ile Gly Ile Asp Lys His Gln Asn Met Gln
305 310 315

(2) INFORMATION FOR SEQ ID NO:10:

.(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 492 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Pro Gln Val Thr Lys Thr Asn Asn Glu Asn Glu Phe Arg Leu Thr
1 5 10 15

Arg Ser Lys Val Gln His Gln Glu Ser Ile Ser Thr Ile Lys Asn Thr
20 25 30

Thr Ile Ser Asn Ser Gln His Lys Gln Gln Thr Gln Gln Gln Ile Ser
35 40 45

Ser Pro Pro Gln Val Ser Val Thr Ser Ser Glu Gly Val Ser His Val
50 55 60

Asn Thr Arg Gln Tyr Leu Gly Asp Val Ser Asn Gln Tyr Ile Thr Asn
65 70 75 80

Ala Lys Pro Thr Asn Lys Arg Lys Pro Leu Gly Gly Asp Asn Ala Pro
85 90 95

Leu Gln Lys Gln Gln His Arg Pro Ser Arg Pro Ile Pro Ile Ala Ser
100 105 110

Asp Asn Asn Asn Asn Gly Ser Thr Ser Ser Ser Ser Asn Ser Ser Asn
115 120 125

Asn Asn Asn Asn Asp Ala Asn Arg Leu Ala Ser Leu Ala Val Pro Ser
130 135 140

Arg Leu Pro Gln Lys Arg Gln Ala Thr Glu Ser Ser Thr Asn Leu Val
145 150 155 160

Glu Lys Leu Arg Val Pro Gln Pro Glu Val Gly Glu Arg Ser Gln Ser
165 170 175

Tyr His Lys Lys Ser Arg Leu Ile Asp Tyr Glu Trp Gln Asp Leu Asp
180 185 190

Glu Glu Asp Asn Asp Asp Gln Leu Met Val Ser Glu Tyr Val Asn Glu
195 200 205

Ile 210	Phe	Ser	Tyr	Tyr	Tyr	Glu 215	Leu	Glu	Thr	Arg	Met 220	Leu	Pro	Asp	Pro
Gln 225	Tyr	Leu	Phe	Lys	Gln 230	Thr	Leu	Leu	Lys	Pro 235	Arg	Met	Arg	Ser	Ile 240
Leu	Val	Asp	Trp	Leu 245	Val	Glu	Met	His	Leu 250	Lys	Phe	Lys	Leu	Leu 255	Pro
Glu	Ser	Leu	Phe 260	Leu	Ala	Val	Asn	Val 265	Met	Asp	Arg	Phe	Met 270	Ser	Val
Glu	Val	Val 275	Gln	Ile	Asp	Lys	Leu 280	Gln	Leu	Leu	Ala	Thr 285	Ala	Ala	Leu
Phe 290	Thr	Ala	Ala	Lys	Asn	Glu 295	Glu	Val	Phe	Ser	Pro 300	Leu	Val	Lys	Asn
Tyr 305	Ala	Tyr	Phe	Thr	Asp 310	Gly	Ser	Tyr	Thr	Pro 315	Glu	Glu	Val	Val	Gln 320
Ala	Glu	Lys	Tyr	Met 325	Leu	Thr	Ile	Leu	Asn 330	Phe	Asp	Leu	Asn	Tyr 335	Pro
Asn	Pro	Met	Asn 340	Phe	Leu	Arg	Arg	Ile 345	Ser	Lys	Ala	Asp	Asp 350	Tyr	Asp
Val	Gln	Ser 355	Arg	Thr	Leu	Gly	Lys 360	Tyr	Leu	Leu	Glu	Ile 365	Thr	Ile	Val
Asp 370	Tyr	Lys	Phe	Ile	Gly	Met 375	Arg	Pro	Ser	Leu	Cys 380	Cys	Ala	Leu	Ala
Met 385	Tyr	Leu	Ala	Arg	Leu 390	Ile	Leu	Gly	Lys	Leu 395	Pro	Val	Trp	Asn	Gly 400
Asn	Leu	Ile	His 405	Tyr	Ser	Gly	Gly	Tyr	Arg 410	Ile	Ser	Asp	Met	Arg 415	Glu
Cys	Ile	Glu	Leu 420	Met	Phe	Gln	Tyr	Leu 425	Ile	Ala	Pro	Ile	Glu 430	His	Asp
Glu	Phe	Phe 435	Lys	Lys	Tyr	Ala	Met 440	Arg	Lys	Phe	Met	Arg 445	Ala	Ser	Thr
Leu 450	Cys	Arg	Asn	Trp	Ala	Lys 455	Lys	Phe	Gln	Ala	Ser 460	Gly	Arg	Asp	Leu
Phe 465	Asp	Glu	Arg	Leu	Ser 470	Thr	His	Arg	Leu	Thr 475	Leu	Glu	Asp	Asp	Asp 480
Glu	Glu	Glu	Glu	Ile 485	Val	Val	Ala	Glu	Ala	Glu	Glu				

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 343 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ser	Thr	Ala	Ala	Val	Ala	Thr	Lys	Pro	Ser	Val	Thr	Ser	Lys	Pro	1	5	10	15
Ala	Thr	Lys	Gln	Val	Leu	Asn	Tyr	Thr	Lys	Glu	Lys	Lys	Val	Gly	Glu	20	25	30	
Gly	Thr	Tyr	Ala	Val	Val	Tyr	Leu	Gly	Lys	Gln	Ile	Ser	Thr	Lys	Arg	35	40	45	
Gln	Ile	Ala	Ile	Lys	Glu	Ile	Lys	Thr	Gly	Leu	Phe	Lys	Asp	Gly	Leu	50	55	60	
Asp	Met	Ser	Ala	Leu	Arg	Glu	Val	Lys	Tyr	Leu	Gln	Glu	Leu	Lys	His	65	70	75	80
Pro	Asn	Val	Ile	Glu	Leu	Val	Asp	Val	Phe	Ser	Ala	Thr	Asn	Asn	Leu	85	90	95	
Asn	Leu	Val	Leu	Glu	Phe	Leu	Pro	Cys	Asp	Leu	Glu	Val	Leu	Ile	Lys	100	105	110	
Asp	Lys	Ser	Ile	Val	Phe	Lys	Ser	Ala	Asp	Ile	Lys	Ser	Trp	Leu	Leu	115	120	125	
Met	Thr	Leu	Arg	Gly	Ile	His	His	Cys	His	Arg	Asn	Phe	Ile	Leu	His	130	135	140	
Arg	Asp	Leu	Lys	Pro	Asn	Asn	Leu	Leu	Leu	Ala	Pro	Asp	Gly	Gln	Leu	145	150	155	160
Lys	Ile	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ala	Leu	Val	Asn	Pro	Asn	Glu	165	170	175	
Asp	Leu	Ser	Ser	Asn	Val	Val	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Leu	180	185	190	
Leu	Phe	Gly	Ala	Arg	His	Tyr	Thr	Gly	Ala	Val	Asp	Ile	Trp	Ser	Ile	195	200	205	
Gly	Ile	Ile	Phe	Ala	Glu	Leu	Met	Leu	Arg	Ile	Pro	Tyr	Leu	Pro	Gly	210	215	220	
Lys	Asp	Asp	Val	Asp	Gln	Leu	Asp	Val	Thr	Phe	Arg	Ala	Tyr	Gly	Thr	225	230	235	240
Pro	Thr	Glu	Gln	Ile	Trp	Pro	Asn	Val	Ser	Ser	Leu	Pro	Met	Tyr	Asn	245	250	255	
Ala	Leu	His	Val	Tyr	Pro	Pro	Pro	Ser	Arg	Gln	Glu	Leu	Arg	Asn	Arg	260	265	270	

Phe Ser Ala Ala Thr Glu Lys Ala Leu Asp Leu Leu Ile Ser Met Thr
 275 280 285
 Gln Leu Asp Pro Ser Arg Arg Cys Asp Ser Thr Leu Ala Leu Leu His
 290 295 300
 Asp Tyr Phe Thr Glu Ser Pro Arg Pro Thr Asp Pro Lys Lys Leu Pro
 305 310 315 320
 Lys Lys Ser Ser Pro Glu Lys Arg Glu Asn Glu Asp Glu Gln Asn Asn
 325 330 335
 Gly Ser Lys Arg Arg His Val
 340

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Cys Ser Ala Ile Asp Thr Lys Ser Ser Val Ser Ala Met Glu His Lys
 1 5 10 15
 Ile Ala Ile Lys Lys Val Thr Lys Ile Phe Asn Lys Asp Ile Leu Leu
 20 25 30
 Ile Arg Ala Ile Arg Glu Leu Lys Phe Met Met Phe Phe Arg Gly His
 35 40 45
 Lys Asn Ile Ala Thr Leu Leu Asp Leu Asp Val Val Tyr Val Lys Pro
 50 55 60
 Tyr Glu Gly Leu Tyr Cys Phe Gln Glu Leu Ala Asp Leu Asp Leu Ala
 65 70 75 80
 Arg Val Leu Tyr Ser Asn Val Gln Phe Ser Glu Phe His Ile Gln Ser
 85 90 95
 Phe Met Tyr Gln Ile Leu Cys Gly Leu Lys Tyr Ile His Ser Ala Asp
 100 105 110
 Val Ile His Arg Asp Leu Lys Pro Gly Asn Ile Leu Val Thr Thr Gln
 115 120 125
 Gly Thr Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Gly Ile Asn Pro
 130 135 140
 Val Tyr Phe Arg Asn Arg Ser Ala Val Ile Thr Asn Tyr Val Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1019 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1017

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG AAG TTG TCA GAT TAT TAT ATA GAC AAG GAA TTA ATT TAC AAT AGT	48
Met Lys Leu Ser Asp Tyr Tyr Ile Asp Lys Glu Leu Ile Tyr Asn Ser	
1 5 10 15	
GCC ATT TCT GAT ATA TAT ACG GCT ATT GAT AAG TTT AAT AAC TTA CCA	96
Ala Ile Ser Asp Ile Tyr Thr Ala Ile Asp Lys Phe Asn Asn Leu Pro	
20 25 30	
GTA TGT CTT AAA ATA GTT GAT GAA GAT TTC AGT CTT CCA CCA CAT TCA	144
Val Cys Leu Lys Ile Val Asp Glu Asp Phe Ser Leu Pro Pro His Ser	
35 40 45	
ATC CAT CGA GAA ATT TTT ATA CTT AAA ACT TTG AAA CCA CAT CCA AAC	192
Ile His Arg Glu Ile Phe Ile Leu Lys Thr Leu Lys Pro His Pro Asn	
50 55 60	
ATA ATT GAA TAT TTT AAT GAT CTT AAA ATT TAT GAT GAT GTT ATA TTA	240
Ile Ile Glu Tyr Phe Asn Asp Leu Lys Ile Tyr Asp Asp Val Ile Leu	
65 70 75 80	
GTC ACC AAA TTG TAT CGT TAT GAT TTG AGT CAA TTG ATT GAA ATT ACA	288
Val Thr Lys Leu Tyr Arg Tyr Asp Leu Ser Gln Leu Ile Glu Ile Thr	
85 90 95	
AAA TAT TGT AAA CGA ACA ACA CGA TTT ATT TAT GGT ATT AAT GGT AAT	336
Lys Tyr Cys Lys Arg Thr Thr Arg Phe Ile Tyr Gly Ile Asn Gly Asn	
100 105 110	
CTT GTT AGT AAT CAA TAT ACA CTT GCT AAT GAA ATT GAA GAA AAA GAT	384
Leu Val Ser Asn Gln Tyr Thr Leu Ala Asn Glu Ile Glu Glu Lys Asp	
115 120 125	
ATC AAA TTA TGG TTA AAA TCA ATG AGT TCA GGA CTT GAA TTT ATT CAT	432
Ile Lys Leu Trp Leu Lys Ser Met Ser Ser Gly Leu Glu Phe Ile His	
130 135 140	
TCA CAA GGG ATA ATT CAT CGT GAT ATA AAA CCC AGT AAT ATT TTC TTT	480
Ser Gln Gly Ile Ile His Arg Asp Ile Lys Pro Ser Asn Ile Phe Phe	
145 150 155 160	

GCC CGG GAT GAT ATA ACA CAA CCG ATT ATT GGA GAT TTT GAT ATT TGT Ala Arg Asp Asp Ile Thr Gln Pro Ile Ile Gly Asp Phe Asp Ile Cys 165 170 175	528
TAT GAT TTA AAA CTG CCA CCT AAA GAT GAA CCC CCT ATG GCG AAA TAT Tyr Asp Leu Lys Leu Pro Pro Lys Asp Glu Pro Pro Met Ala Lys Tyr 180 185 190	576
ATT GAT GTA TCT ACA GGT ATT TAT AAA GCA CCA GAA TTG ATT CTT GGT Ile Asp Val Ser Thr Gly Ile Tyr Lys Ala Pro Glu Leu Ile Leu Gly 195 200 205	624
ATA ACT AAT TAT GAA TAT GAA ATT GAT ATT TGG TCA TTG GGT ATA ATT Ile Thr Asn Tyr Glu Tyr Glu Ile Asp Ile Trp Ser Leu Gly Ile Ile 210 215 220	672
TTG ACT GGT TTA TAT TCA GAA AAT TTT CAA AGT GTT TTA GTC AAA GAT Leu Thr Gly Leu Tyr Ser Glu Asn Phe Gln Ser Val Leu Val Lys Asp 225 230 235 240	720
GAT AAA GAA TTG ACT AAT GAT TCT CAT GTT AGT GAT TTA TAT TTA TTA Asp Lys Glu Leu Thr Asn Asp Ser His Val Ser Asp Leu Tyr Leu Leu 245 250 255	768
AAT CAA ATA TTT GAA AAT TTC GGT ACA CCC AAT TTA ACT GAT TTT GAA Asn Gln Ile Phe Glu Asn Phe Gly Thr Pro Asn Leu Thr Asp Phe Glu 260 265 270	816
GAT GAA TTA TTT TGT GAT GAA TAT AAT AAT GAA AAC TTG CAT TTT AAA Asp Glu Leu Phe Cys Asp Glu Tyr Asn Asn Glu Asn Leu His Phe Lys 275 280 285	864
AAA TTC AAT TTA CAA AAA TAT CCT AGA AAA GAT TGG GAT ATT ATT TTA Lys Phe Asn Leu Gln Lys Tyr Pro Arg Lys Asp Trp Asp Ile Ile Leu 290 295 300	912
CCT CGA TGC AAT GAT GAT TTA ATG AAA GAA ATT TTT ACC AAG ATG ATT Pro Arg Cys Asn Asp Asp Leu Met Lys Glu Ile Phe Thr Lys Met Ile 305 310 315 320	960
AGA TAT GAT CGA AGT AAA AGA ATA ACT TCT AAA GAA ATC TTA CAA TTA Arg Tyr Asp Arg Ser Lys Arg Ile Thr Ser Lys Glu Ile Leu Gln Leu 325 330 335	1008
ATG TTG GAT TG Met Leu Asp	1019

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Lys	Leu	Ser	Asp	Tyr	Tyr	Ile	Asp	Lys	Glu	Leu	Ile	Tyr	Asn	Ser	1	5	10	15
Ala	Ile	Ser	Asp	Ile	Tyr	Thr	Ala	Ile	Asp	Lys	Phe	Asn	Asn	Leu	Pro	20	25	30	
Val	Cys	Leu	Lys	Ile	Val	Asp	Glu	Asp	Phe	Ser	Leu	Pro	Pro	His	Ser	35	40	45	
Ile	His	Arg	Glu	Ile	Phe	Ile	Leu	Lys	Thr	Leu	Lys	Pro	His	Pro	Asn	50	55	60	
Ile	Ile	Glu	Tyr	Phe	Asn	Asp	Leu	Lys	Ile	Tyr	Asp	Asp	Val	Ile	Leu	65	70	75	80
Val	Thr	Lys	Leu	Tyr	Arg	Tyr	Asp	Leu	Ser	Gln	Leu	Ile	Glu	Ile	Thr	85	90	95	
Lys	Tyr	Cys	Lys	Arg	Thr	Thr	Arg	Phe	Ile	Tyr	Gly	Ile	Asn	Gly	Asn	100	105	110	
Leu	Val	Ser	Asn	Gln	Tyr	Thr	Leu	Ala	Asn	Glu	Ile	Glu	Glu	Lys	Asp	115	120	125	
Ile	Lys	Leu	Trp	Leu	Lys	Ser	Met	Ser	Ser	Gly	Leu	Glu	Phe	Ile	His	130	135	140	
Ser	Gln	Gly	Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Phe	Phe	145	150	155	160
Ala	Arg	Asp	Asp	Ile	Thr	Gln	Pro	Ile	Ile	Gly	Asp	Phe	Asp	Ile	Cys	165	170	175	
Tyr	Asp	Leu	Lys	Leu	Pro	Pro	Lys	Asp	Glu	Pro	Pro	Met	Ala	Lys	Tyr	180	185	190	
Ile	Asp	Val	Ser	Thr	Gly	Ile	Tyr	Lys	Ala	Pro	Glu	Leu	Ile	Leu	Gly	195	200	205	
Ile	Thr	Asn	Tyr	Glu	Tyr	Glu	Ile	Asp	Ile	Trp	Ser	Leu	Gly	Ile	Ile	210	215	220	
Leu	Thr	Gly	Leu	Tyr	Ser	Glu	Asn	Phe	Gln	Ser	Val	Leu	Val	Lys	Asp	225	230	235	240
Asp	Lys	Glu	Leu	Thr	Asn	Asp	Ser	His	Val	Ser	Asp	Leu	Tyr	Leu	Leu	245	250	255	
Asn	Gln	Ile	Phe	Glu	Asn	Phe	Gly	Thr	Pro	Asn	Leu	Thr	Asp	Phe	Glu	260	265	270	
Asp	Glu	Leu	Phe	Cys	Asp	Glu	Tyr	Asn	Asn	Glu	Asn	Leu	His	Phe	Lys	275	280	285	
Lys	Phe	Asn	Leu	Gln	Lys	Tyr	Pro	Arg	Lys	Asp	Trp	Asp	Ile	Ile	Leu	290	295	300	

Pro Arg Cys Asn Asp Asp Leu Met Lys Glu Ile Phe Thr Lys Met Ile
 305 310 315 320

Arg Tyr Asp Arg Ser Lys Arg Ile Thr Ser Lys Glu Ile Leu Gln Leu
 325 330 335

Met Leu Asp

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATGGATCCYT TRTANCCNCC RTSNARNANR TANAYNTCNG GRTA

44

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGATCCAT NATNGAYTGY MGNTWYCCNT AYGA

34

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATGGATCCAT NATNGAYTGY MGNTWYGANT AYGA

34

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TWYGARTAYM GNCA YGTNAT G

21

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AANARNARDA TRTGNGGYTC

20

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNGGNGCNC KRTACCANAR NGT

23

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGNGARGGNA CNTAYGGNGT NGT

23

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GANGANYKNG MNGANCCNYT NATG

24

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATNCKNCKNA RRAARTTCAT

20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GACCAACACG AATTCCAAAT GGTAGAGTTA TCTG

34

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TGAGGAGTCG ACCAAGATTT ATTGCATG

28

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CATTTTGAAT TCATAGTAAT GCCACAAGTC

30

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATAGTCCTCG AGACTTTACT CTTCTGCTTC

30